



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/368,989

DATE: 07/14/2003

TIME: 14:12:41

Input Set : N:\EBONY'S\368989.txt

Output Set: N:\CRF4\07142003\I368989.raw

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Fred J. Stevens

7 Marianne Schiffer

8 Priscilla Wilkins-Stevens

9 W. Carey Hanly

10 Sandra L. Tollaksen

11 (ii) TITLE OF INVENTION: DEVICE FOR DETECTING MOLECULES, METHOD FOR
12 DETECTING MOLECULES

13 (iii) NUMBER OF SEQUENCES: 5

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: CHERSKOV & FLAYNIK

16 (B) STREET: 20 N. Wacker Drive

17 (C) CITY: Chicago

18 (D) STATE: Illinois

19 (E) COUNTRY: United States

20 (F) ZIP: 60606

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: compact disc

23 (B) COMPUTER: PC

24 (C) OPERATING SYSTEM: Microsoft Windows XP

25 (D) SOFTWARE: Wordperfect

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/368,989

C--> 28 (B) FILING DATE: 05-Aug-1999

29 (viii) ATTORNEY/AGENT INFORMATION:

30 (A) NAME: Cherskov, Michael J.

31 (B) REGISTRATION NUMBER: 33,664

32 (C) REFERENCE/DOCKET NUMBER: 0003/00332

33 (ix) TELECOMMUNICATION INFORMATION:

34 (A) TELEPHONE: (312) 621-1330

35 (B) TELEFAX: (312) 621-0088

do not
Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

38 (2) INFORMATION FOR SEQ ID NO: 1:

39 (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 111 amino acids

41 (B) TYPE: amino acid

42 (C) STRANDEDNESS: Single

43 (D) TOPOLOGY: linear

44 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

P.2

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```

46  Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Pro
47  1 5 10 15
49  Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Leu Leu
E--> 50  20 20 25 25 30 30
52  Asp Ala Ser Phe Asp Thr Asn Thr Leu Ala Trp Tyr Gln Gln Lys
E--> 53  35 40 45
55  Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ser Arg
E--> 56  50 55 60
58  Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
E--> 59  65 70 75
61  Asp Phe Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
E--> 62  80 85 90
64  Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly
E--> 65  95 100 105
67  Thr Lys Leu Glu Ile Lys
E--> 68  110
71 (2) INFORMATION FOR SEQ ID NO: 2
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 111 amino acids
74 (B) TYPE: amino acid
75 (C) STRANDEDNESS: Single
76 (D) TOPOLOGY: linear
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
79  Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
80  1 5 10 15
82  Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu
E--> 83  20 25 30
85  Tyr Ser Ser Asn Ser Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
E--> 86  35 40 45
88  Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
E--> 89  50 55 60
91  Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
E--> 92  65 70 75
94  Asp Phe Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
E--> 95  80 85 90
97  Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly
E--> 98  95 100 105
100  Thr Lys Leu Glu Ile Lys
E--> 101  110
104 (2) INFORMATION FOR SEQ ID NO: 3
105 (i) SEQUENCE CHARACTERISTICS:
106 (A) LENGTH: 111 amino acids
107 (B) TYPE: amino acid
108 (C) STRANDEDNESS: Single
109 (D) TOPOLOGY: linear
110 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
112  Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
113  1 5 10 15
115  Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu

```

*misaligned
amino acid
numbers
(see item 3
on Enon
summary sheet)*

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Input Set : N:\EBONY'S\368989.txt

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```

E--> 116      20      25      30
118 Tyr Ser Ser Asn Ser Thr Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
E--> 119      35      40      45
121 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
E--> 122      50      55      60
124 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
E--> 125      65      70      75
127 Asp Phe Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
E--> 128      80      85      90
130 Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly
E--> 131      95     100     105
133 Thr Lys Leu Glu Ile Lys

```

```

E--> 134      110
137 (2) INFORMATION FOR SEQ ID NO: 4:
138 (i) SEQUENCE CHARACTERISTICS:
139 (A) LENGTH: 111 amino acids
140 (B) TYPE: amino acid
141 (C) STRANDEDNESS: Single
142 (D) TOPOLOGY: linear
143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
145 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
146 1 5 10 15
148 Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu
E--> 149      20      25      30
151 Tyr Ser Ser Asn Ser Lys Asn Tyr Leu Ala Trp Tyr Gln Glu Lys
E--> 152      35      40      45
154 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
E--> 155      50      55      60
157 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
E--> 158      65      70      75
160 Asp Phe Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
E--> 161      80      85      90
163 Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly
E--> 164      95     100     105
166 Thr Lys Leu Glu Ile Lys
E--> 167      110

```

```

170 (2) INFORMATION FOR SEQ ID NO: 5:
171 (i) SEQUENCE CHARACTERISTICS:
172 (A) LENGTH: 111 amino acids
173 (B) TYPE: amino acid
174 (C) STRANDEDNESS: Single
175 (D) TOPOLOGY: linear
176 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
178 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
179 1 5 10 15
181 Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu
E--> 182      20      25      30
184 Tyr Ser Ser Asn Ser Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
E--> 185      35      40      45

```

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Input Set : N:\EBONY'S\368989.txt

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187	Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg	
E--> 188	50	55 60
190	Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr	
E--> 191	65	70 75
193	Asp Phe Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr	
E--> 194	80	85 90
196	Tyr Cys Leu Gln Tyr Tyr Ser Thr Pro Tyr Ser Phe Gly Gln Gly	
E--> 197	95	100 105
199	Thr Lys Leu Glu Ile Lys	
E--> 200	110	

VERIFICATION SUMMARYPATENT APPLICATION: **US/09/368,989**

DATE: 07/14/2003

TIME: 14:12:42

Input Set : **N:\EBONY'S\368989.txt**Output Set: **N:\CRF4\07142003\I368989.raw**

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:50 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=1
L:83 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:116 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
M:332 Repeated in SeqNo=3
L:149 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:182 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5